



SEQUENCE LISTING

<110> Logemann, Juergen  
Jach, Guido  
Gornhardt, Birgit  
Mundy, John  
Schell, Jeff  
Eckes, Peter  
Chet, Ilan

<120> Transgenic pathogen-resistant organism

<130> A29542-FWC-I-R 070037.0195

<140> US 09/729,141

<141> 2000-12-01

<150> 08/812,025

<151> 1997-03-06

<150> 08/457,797

<151> 1995-06-01

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<151> 1993-10-08

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Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp

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5	10	15	20	
aat atc tgc aag tac aag gca cag agc ggc aag act gcc att tgc aag	153			
Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys				
25 30 35				
tgc tat gtc aaa aag tgc ccc cgc gac ggc gcg aaa tgc gag ttt gac	201			
Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp				
40 45 50				
agc tac aag ggg aag tgc tac tgc tagacggtga gcgaagggac gaagtaggct	255			
Ser Tyr Lys Gly Lys Cys Tyr Cys				
55 60				
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 Met Ala Lys Asn Val Asp Lys Pro Leu Phe Thr Ala Thr Phe Asn Val  
 5 10 15 20  
 cag gcc agc tcc gcc gac tac gcc acc ttc atc gcc ggc atc cgc aac 150  
 Gln Ala Ser Ser Ala Asp Tyr Ala Thr Phe Ile Ala Gly Ile Arg Asn  
 25 30 35  
 aag ctc cgc aac ccg gcg cac ttc tcc cac aac cgc ccc gtg ctg ccg 198  
 Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg Pro Val Leu Pro  
 40 45 50

ccg gtc gag ccc aac gtc ccg ccg agc agg tgg ttc cac gtc gtg ctc	246
Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe His Val Val Leu	
55 60 65	
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Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala Ile Arg Ala Asp	
70 75 80	
aac atc tac ctg gag ggc ttc aag agc agc gac ggc acc tgg tgg gag	342
Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly Thr Trp Trp Glu	
85 90 95 100	
ctc acc ccg ggc ctc atc ccc ggc gcc acc tac gtc ggg ttc ggc ggc	390
Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val Gly Phe Gly Gly	
105 110 115	
acc tac cgc gac ctc ctc ggc gac acc gac aag ctg acc aac gtc gct	438
Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu Thr Asn Val Ala	
120 125 130	
ctc ggc cgg cag cag ctg gcg gac gcg gtg acc gcc ctc cac ggg cgc	486
Leu Gly Arg Gln Gln Leu Ala Asp Ala Val Thr Ala Leu His Gly Arg	
135 140 145	
acc aag gcc gac aag ccg tcc ggc ccg aag cag cag cag gcg agg gag	534
Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln Gln Ala Arg Glu	
150 155 160	
gcg gtg acg acg ctg ctc ctc atg gtg aac gag gcc acg cgg ttc cag	582
Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln	
165 170 175 180	
acg gtg tct ggg ttc gtg gcc ggg ttg ctg cac ccc aag gcg gtg gag	630
Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu	
185 190 195	
aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg	678
Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly	
200 205 210	
tgg cag gac ctg tcc gcg gcg ctg ctg aag acg gac gtg aag cct ccg	726
Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro	
215 220 225	
ccg gga aag tcg cca gcg aag ttc gcg ccg atc gag aag atg ggc gtg	774
Pro Gly Lys Ser Pro Ala Lys Phe Ala Pro Ile Glu Lys Met Gly Val	
230 235 240	

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agg acg gct gta cag gcc gcc aac acg ctg ggg atc ctg ctg ttc gtg 822
Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile Leu Leu Phe Val
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gag gtg ccg ggt ggg ttg acg gtg gcc aag gcg ctg gag ctg ttc cat 870
Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu Glu Leu Phe His
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gcg agt ggt ggg aaa taggtagttt tccaggtata cctgcatggg tagtgtaaaa 925
Ala Ser Gly Gly Lys
                280

gtcgaataaa catgtcacag agtgacggac tgatataaat aaataaataa acgtgtcaca 985
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<210> 5
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<212> PRT
<213> Hordeum vulgare

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Gly Ile Arg Asn Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg
          35          40          45
Pro Val Leu Pro Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe
          50          55          60
His Val Val Leu Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala
65          70          75          80
Ile Arg Ala Asp Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly
          85          90          95
Thr Trp Trp Glu Leu Thr Pro Gly Leu Ile Pro Gly Ala Thr Tyr Val
          100         105         110
Gly Phe Gly Gly Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu
          115         120         125
Thr Asn Val Ala Leu Gly Arg Gln Gln Leu Ala Asp Ala Val Thr Ala
          130         135         140
Leu His Gly Arg Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln
145          150         155         160
Gln Ala Arg Glu Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala
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Thr Arg Phe Gln Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro
          180         185         190
Lys Ala Val Glu Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala
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Gln Val Asn Gly Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp

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210		215		220	
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225		230		235	240
Lys Met Gly Val Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile					
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 <213> Hordeum vulgare

<220>  
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 <222> (1)...(351)  
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 incomplete protein from an incomplete PSI cDNA  
 clone

<221> 3'UTR  
 <222> (352)...(487)

<221> polyA\_signal  
 <222> (404)...(409)  
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 1 5 10 15  
  
 acg gtg tcg ggg ttc gtg gcc ggg ctg ctg cac ccc aag gcg gtg gag 96  
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 aag aag agc ggg aag atc ggc aat gag atg aag gcc cag gtg aac ggg 144



<210> 8  
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<212> DNA  
<213> *Serratia marcescens*

<220>  
<221> misc\_feature  
<222> (1)...(2329)  
<223> ChiS gene from plasmid pLChis from E.coli A5187

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cttttttatt tatagtactg aatgtacgcg gtgggaatga ttatttcgcc acgtggaaag 240  
acgctggtgt tatttattga ttttaacctt cgcggattat tgcggaattt tttcgcttcg 300  
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aaaaataacc gttcagatat tcatcattca gcaacaaagt tttggcgttt tttaacggag 2280
ttaaaaacca gtaagtttgt gagggtcaga ccaatgcgct aaaaatggg 2329

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<211> 1002

<212> DNA

<213> Hordeum vulgare

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<222> (64)...(861)

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<222> (905)...(910)

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<221> sig\_peptide

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<222> (349)...(378)

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<222> (466)...(588)

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<222> (133)...(861)

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Met Arg Ser Leu Ala Val Val Val Ala Val Val Ala Thr Val Ala	
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atg gcc atc ggc acg gcg cgc ggc agc gtg tcc tcc atc gtc tcg cgc	156
Met Ala Ile Gly Thr Ala Arg Gly Ser Val Ser Ser Ile Val Ser Arg	
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gca cag ttt gac cgc atg ctt ctc cac cgc aac gac ggc gcc tgc cag	204
Ala Gln Phe Asp Arg Met Leu Leu His Arg Asn Asp Gly Ala Cys Gln	
35 40 45	
gcc aag ggc ttc tac acc tac gac gcc ttc gtc gcc gcc gca gcc gcc	252
Ala Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala Ala	
50 55 60	
ttc ccg ggc ttc ggc acc acc ggc agc gcc gac gcc cag aag cgc gag	300
Phe Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Ala Gln Lys Arg Glu	
65 70 75	
gtg gcc gcc ttc cta gca cag acc tcc cac gag acc acc ggc ggg tgg	348
Val Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr Thr Gly Gly Trp	
80 85 90 95	
gcg act gca ccg gac ggg gcc ttc gcc tgg ggc tac tgc ttc aag cag	396
Ala Thr Ala Pro Asp Gly Ala Phe Ala Trp Gly Tyr Cys Phe Lys Gln	
100 105 110	
gaa cgt ggc gcc tcc tcc gac tac tgc acc ccg agc gca caa tgg ccg	444
Glu Arg Gly Ala Ser Ser Asp Tyr Cys Thr Pro Ser Ala Gln Trp Pro	
115 120 125	
tgc gcc ccc ggg aag cgc tac tac ggc cgc ggg cca atc cag ctc tcc	492
Cys Ala Pro Gly Lys Arg Tyr Tyr Gly Arg Gly Pro Ile Gln Leu Ser	
130 135 140	
cac aac tac aac tat gga cct gcc ggc cgg gcc atc ggg gtc gat ctg	540
His Asn Tyr Asn Tyr Gly Pro Ala Gly Arg Ala Ile Gly Val Asp Leu	
145 150 155	
ctg gcc aac ccg gac ctg gtg gcc acg gac gcc act gtg ggc ttt aag	588
Leu Ala Asn Pro Asp Leu Val Ala Thr Asp Ala Thr Val Gly Phe Lys	
160 165 170 175	

acg gcc atc tgg ttc tgg atg acg gcg cag ccg ccc aag cca tcg agc 636  
 Thr Ala Ile Trp Phe Trp Met Thr Ala Gln Pro Pro Lys Pro Ser Ser  
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cat gct gtg atc gcc ggc cag tgg agc ccg tca ggg gct gac cgg gcc 684  
 His Ala Val Ile Ala Gly Gln Trp Ser Pro Ser Gly Ala Asp Arg Ala  
                   195                  200                  205

gca ggc cgg gtg ccc ggg ttt ggt gtg atc acc aac atc atc aac ggc 732  
 Ala Gly Arg Val Pro Gly Phe Gly Val Ile Thr Asn Ile Ile Asn Gly  
                   210                  215                  220

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 Gly Ile Glu Cys Gly His Gly Gln Asp Ser Arg Val Ala Asp Arg Ile  
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ggg ttt tac aag cgc tac tgt gac atc ctc ggc gtt ggc tac ggc aac 828  
 Gly Phe Tyr Lys Arg Tyr Cys Asp Ile Leu Gly Val Gly Tyr Gly Asn  
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aac ctc gat tgc tac agc cag aga ccc ttc gcc taattaatta gtcattgtatt 881  
 Asn Leu Asp Cys Tyr Ser Gln Arg Pro Phe Ala  
                   260                  265

aatcttggcc ctccataaaa tacaataaga gcacgtctc ctatctacat gctgtaagat 941  
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 a 1002

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<212> PRT

<213> Hordeum vulgare

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 Gln Phe Asp Arg Met Leu Leu His Arg Asn Asp Gly Ala Cys Gln Ala  
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 Lys Gly Phe Tyr Thr Tyr Asp Ala Phe Val Ala Ala Ala Ala Phe  
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 Pro Gly Phe Gly Thr Thr Gly Ser Ala Asp Ala Gln Lys Arg Glu Val  
 65                  70                  75                  80  
 Ala Ala Phe Leu Ala Gln Thr Ser His Glu Thr Thr Gly Gly Trp Ala  
                   85                  90                  95

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Asn	Tyr	Asn	Tyr	Gly	Pro	Ala	Gly	Arg	Ala	Ile	Gly	Val	Asp	Leu	Leu	
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Phe	Tyr	Lys	Arg	Tyr	Cys	Asp	Ile	Leu	Gly	Val	Gly	Tyr	Gly	Asn	Asn	
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			260					265								

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 <222> (1210)...(1215)  
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<221> mat\_peptide

<222> (133)...(1050)

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Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile Gly Ala Phe  
5 10 15

gct gct gtt cct acg agt gtg cag tcc atc ggc gta tgc tac ggc gtg 153  
Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys Tyr Gly Val  
20 25 30 35

atc ggc aac aac ctc ccc tcc cgg agc gac gtg gtg cag ctc tac agg 201  
Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln Leu Tyr Arg  
40 45 50

tcc aag ggc atc aac ggc atg cgc atc tac ttc gcc gac ggg cag gcc 249  
Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp Gly Gln Ala  
55 60 65

ctc tcg gcc gtc cgc aac tcc ggc atc ggc ctc atc ctc gac atc ggc 297  
Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu Asp Ile Gly  
70 75 80

aac gac cag ctc gcc aac atc gcc gcc agc acc tcc aac gcg gcc tcc 345  
Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn Ala Ala Ser  
85 90 95

tgg gtc cag aac aac gtg cgg ccc tac tac cct gcc gtg aac atc aag 393  
Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val Asn Ile Lys  
100 105 110 115

tac atc gcc gcc ggc aac gag gtg cag ggc ggc gcc acg cag agc atc 441  
Tyr Ile Ala Ala Gly Asn Glu Val Gln Gly Gly Ala Thr Gln Ser Ile  
120 125 130

ctg ccg gcc atg cgc aac ctc aac gcg gcc ctc tcc gcg gcg ggg ctc 489  
Leu Pro Ala Met Arg Asn Leu Asn Ala Ala Leu Ser Ala Ala Gly Leu  
135 140 145

ggc gcc atc aag gtg tcc acc tcc atc cgg ttc gac gag gtg gcc aac 537  
Gly Ala Ile Lys Val Ser Thr Ser Ile Arg Phe Asp Glu Val Ala Asn  
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tcc ttc ccg ccc tcc gcc ggc gtg ttc aag aac gcc tac atg acg gac	585
Ser Phe Pro Pro Ser Ala Gly Val Phe Lys Asn Ala Tyr Met Thr Asp	
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gtg gcc cgg ctc ctg gcg agc acc ggc gcg ccg ctg ctc gcc aac gtc	633
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180 185 190 195	
tac ccc tac ttc gcg tac cgt gac aac ccc ggg agc atc agc ctg aac	681
Tyr Pro Tyr Phe Ala Tyr Arg Asp Asn Pro Gly Ser Ile Ser Leu Asn	
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tac gcg acg ttc cag ccg ggc acc acc gtg cgt gac cag aac aac ggg	729
Tyr Ala Thr Phe Gln Pro Gly Thr Thr Val Arg Asp Gln Asn Asn Gly	
215 220 225	
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Leu Thr Tyr Thr Ser Leu Phe Asp Ala Met Val Asp Ala Val Tyr Ala	
230 235 240	
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Ala Leu Glu Lys Ala Gly Ala Pro Ala Val Lys Val Val Val Ser Glu	
245 250 255	
agc ggg tgg ccg tcg gcg ggc ggg ttt gcg gcg tcg gcc ggc aat gcg	873
Ser Gly Trp Pro Ser Ala Gly Gly Phe Ala Ala Ser Ala Gly Asn Ala	
260 265 270 275	
cgg acg tac aac cag ggg ctg atc aac cac gtc ggc ggg ggc acg ccc	921
Arg Thr Tyr Asn Gln Gly Leu Ile Asn His Val Gly Gly Gly Thr Pro	
280 285 290	
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Lys Lys Arg Glu Ala Leu Glu Thr Tyr Ile Phe Ala Met Phe Asn Glu	
295 300 305	
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Asn Gln Lys Thr Gly Asp Ala Thr Glu Arg Ser Phe Gly Leu Phe Asn	
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Pro Asp Lys Ser Pro Ala Tyr Asn Ile Gln Phe	
325 330	
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 <211> 334  
 <212> PRT  
 <213> Hordeum vulgare

<400> 12

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			20					25					30		
Tyr	Gly	Val	Ile	Gly	Asn	Asn	Leu	Pro	Ser	Arg	Ser	Asp	Val	Val	Gln
		35					40					45			
Leu	Tyr	Arg	Ser	Lys	Gly	Ile	Asn	Gly	Met	Arg	Ile	Tyr	Phe	Ala	Asp
	50					55					60				
Gly	Gln	Ala	Leu	Ser	Ala	Val	Arg	Asn	Ser	Gly	Ile	Gly	Leu	Ile	Leu
65					70					75					80
Asp	Ile	Gly	Asn	Asp	Gln	Leu	Ala	Asn	Ile	Ala	Ala	Ser	Thr	Ser	Asn
			85						90					95	
Ala	Ala	Ser	Trp	Val	Gln	Asn	Asn	Val	Arg	Pro	Tyr	Tyr	Pro	Ala	Val
			100					105					110		
Asn	Ile	Lys	Tyr	Ile	Ala	Ala	Gly	Asn	Glu	Val	Gln	Gly	Gly	Ala	Thr
		115					120					125			
Gln	Ser	Ile	Leu	Pro	Ala	Met	Arg	Asn	Leu	Asn	Ala	Ala	Leu	Ser	Ala
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Ala	Gly	Leu	Gly	Ala	Ile	Lys	Val	Ser	Thr	Ser	Ile	Arg	Phe	Asp	Glu
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Val	Ala	Asn	Ser	Phe	Pro	Pro	Ser	Ala	Gly	Val	Phe	Lys	Asn	Ala	Tyr
				165					170					175	
Met	Thr	Asp	Val	Ala	Arg	Leu	Leu	Ala	Ser	Thr	Gly	Ala	Pro	Leu	Leu
			180					185					190		
Ala	Asn	Val	Tyr	Pro	Tyr	Phe	Ala	Tyr	Arg	Asp	Asn	Pro	Gly	Ser	Ile
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Ser	Leu	Asn	Tyr	Ala	Thr	Phe	Gln	Pro	Gly	Thr	Thr	Val	Arg	Asp	Gln
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Asn	Asn	Gly	Leu	Thr	Tyr	Thr	Ser	Leu	Phe	Asp	Ala	Met	Val	Asp	Ala
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Val	Tyr	Ala	Ala	Leu	Glu	Lys	Ala	Gly	Ala	Pro	Ala	Val	Lys	Val	Val
				245					250					255	
Val	Ser	Glu	Ser	Gly	Trp	Pro	Ser	Ala	Gly	Gly	Phe	Ala	Ala	Ser	Ala
			260					265					270		
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		275					280					285			
Gly	Thr	Pro	Lys	Lys	Arg	Glu	Ala	Leu	Glu	Thr	Tyr	Ile	Phe	Ala	Met
	290					295					300				
Phe	Asn	Glu	Asn	Gln	Lys	Thr	Gly	Asp	Ala	Thr	Glu	Arg	Ser	Phe	Gly
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Leu	Phe	Asn	Pro	Asp	Lys	Ser	Pro	Ala	Tyr	Asn	Ile	Gln	Phe		

325

330